ANTIGEN 1

100 rccacaa P Q 30	200 ACCTTTA T F S	300 GTCAGGA C E	400 TTAACAA	500 CGAATCC	600 TACAGATC	700 PAACCAA	800 TTTGAAC
90 CAATGAGCAA M S N	190 CAAAAAATTG K K L 60	F O	380 390 400 TTACAAGTACAAATGAGAAATTAACAA L Q V Q M R N 125	490 AACATTAACT	590 CGTTTGGAAT	680 690 TGCAAATTGATGATGCCTT	790 BAATGTTTG
80 GAAAAACAGT' E K Q S 25	180 CAGATGAATT D E F	280 ACATCTATTA H L L 90	380 TTACAAGTAC2 L Q V Q 125	480 ACAATGCGAT	580 MACTGTTAAT		780 rccaagcgga(
70 AAATATGGAG N M E 20	170 GAAATGATTA E M I T	270 AACGTGATAT RDI	370 PAAGGAACTTC RNF 120	460 470 480 490 AAGTGACTAAATTAAACAATGCGATAACATTAAC	570 CAATTGCAAAC	670 AAAACATAGCT	770 AAGAGAGAAA
60 70 80 90 100 TTTTACTACATTAAATATGGGGAAAACAGTCAATGAGCAATCCACAA F T T L N M E E K Q S M S N P Q 20 25 30	160 ATAAAATATTT K I F 50	260 AGAACCGATCG, E P I E 85	360 AAACAAATGT7 K Q M L		550 560 570 580 590 TAACTAATGCAGTTACTCAATTGCAAACAACTGTTAATCGTTTGGAA	630 640 650 660 670 TACACCAGATAACTTACAATAAGAGCGCCCCAAAACATAGCT7	760 TCAATCAGAT
50 CACATCTATTT T S I F 15	150 GGTTTAAATG G L N D	250 3CAAGTATTT/ K Y L 80	350 TCTAAAATTG L K L] 115	450 GCGTTCGTGAA?	550 CATTAACTAA	650 AATTACAATA	750 TAACTCTATC
30 40 50 RAGATCAAATTTACTTACATCTATT RSNLLLTSI RSNLLLTSI	140 CAAAGATTCT(K D S (240 TCAGCAATTA S A I S	340 CAATGAAATT M K F 115	440 GAATCTAGAA	530 CAGATTCATTTGGGACAI	640 CAGATAACTC	740 TGGATCAATC
30 TCTGATAGAT S D R S	130 ATACCAACCA I T N H 40	230 TTCGGTTTCT S V S	330 PATGTTAATAT M L I S	430 GCTTGTTGGC	530 FAGTAGCAGAT	630 acgtcttacac	730 SATAGCAATTC
20 BAGAATTACCA E L P	120 BAATACAAGCAAT N T S N	220 GAATTAAATGA E L N D	320 ICTGTTGATAATTATGTT L L I I M L 105	420 TGTATTTCGA(520 TTACTCAAG	620 ACCACTAAAA	720 CGGCATTTCG
10 20 GAATTCGGCACGAGAATTACCATCTGA1 A R E L P S D 5	110 120 140 150 200 TCGAAAAATACGAATACCAACCACCAAAGATTCTGGTTTAAATGATAAATTTTGAAATGATTACAGATGAATTCAAAAAATTGACCTTTA S K N T N T S N T N H K D S G L N D K I F E M I T D E F K K L T F S 35 40 45 50	210 220 240 250 260 270 290 290 290 250 210 280 290 290 200 210 280 290 290 200 210 280 290 200 200 200 200 200 200 200 200 20	310 320 340 350 370 ATCGAGAAGTCTGTTGATATTTAATATCAATGAAATTTCTAAAATTGAAAATGAAATTTAAGGAACTT SRSLLIMLISMKFLK KUKQMLRNF 100 105 115 115	410 420 430 440 GCATCGACTTGTATTTCGAGGCTTGTTGGCGAATCTAGAAGCGT	510 520 AATAGACAACTTTACTCAAG TAGTAG	610 620 AGTAATGGAATACCACTAAAAACGTCT	710 720 730 750 760 770 780 790 790 710 720 720 770 780 790 790 790 790 790 790

FIG. 1A

FIG. 1B

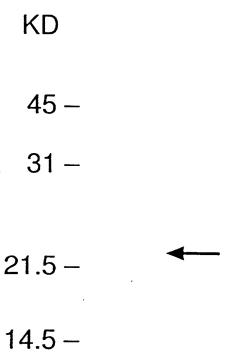
ANTIGEN 2

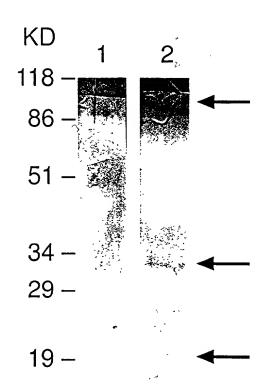
10 20 30 40 50 60 70 80 90 100 GAATTCGCCACGAGATTTTTTTTTTTTTTTTTTTTTTTT	110 120 130 140 150 200 200 CGGAATTTTGAAATTTTGAGCTTTGATAATTTTGATTAGTTTGGTTTTTTTT	210 220 240 250 300 300 AAACACGCTCTTGAAGTTATTCTATTTTTTTTTTTTTTT	310 320 340 360 400 GCGCTGAGAATAATAATATTATCTTTTCTTACATGGAATAAATA	410 420 440 450 500 500 500 CATICTTGGAGAAAATTTCTCTTGAAAGTTCCGGAGAAAACTCTCCACAATTGGATATTGGAGTATTTGGAGTATTTTTTTT	510 520 530 600 600 ATCGATGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	610 620 630 640 650 660 670 680 690 700 CCACTAAACTCAACAATCCAGAATCATAACTTAACTCAGAACCAAAACCACAAAGCCTCATCCAGTTGTTAGACCGCATCCTACAGAAAAGC
GAATTC	CGGAAT G I	AAACAC K H 65	GCGCTC A B	CATTC. I L	ATCGA: I D 65	CCACT

FIG. 2A

7	710 720 790 800 CCTCAAATGGTGAAAGCAAGCCCCTATTACCTCACAGAAAACGAATCAAGTTCAAATCATCCTTCTGTGACAGTTCCAGA	740 AGCCCCTA	750 TTACCTCACC	760 CAGAAAACGAA	, , y atcaagttcaa	ATCATCCTTC	TGTGACAGTI	CCAGA
CTG	830	840	850	860	810 820 830 840 850 860 870 880 890 900	880	890	900
	TTACTATTCC	AGAGACTG	GATCAGACTC	CAGATCACGCG	TACTGGATCAGTTCAAATCTCCTTGTTACTATTCCAGAGACTGGATCAGATCACGCGCCTTGTGACAATTCCAGAGACTGGATCAGTTCAAA	ATTCCAGAGA	ACTGGATCAGI	TCAAA
9.	930	940	950	960	910 920 930 950 950 960 970 970 990 10000 TCATCTTCTCTGCTACTTTCTCCAGAAGATTGGACTTAGAACGTTACCAATCACTTCT	980	990	1000
ACAG	GGATCCAGCT	CAGATCAC	ACTCTGCTAC	CTTCTCCAGAA		ACTCAGAACG	STTACCAATC2	CTTCT
1030	o	1040	1050	1060	1010 1020 1030 1040 1050 1060 1070 1070 1090 1100	1080	1090	1100
ACATATO	CCTAACCA	AAGAAAATG	AAAATCAT <u>AA</u>	<u>ATAA</u> TCAGGAA	ACAGAACAAACTCAAAAGCCAGCTACATATCCTAACCAAGAAATGAAATCCATAATACAGGAAGGTAATTCGAGTTTTAATACACTAAATCTTCCAAA	GTTTTAATAC	CACTAAATCT7	CCAAA
1130)	1140	1150	1160	1110 1120 1130 1140 1150 1160 1170 1170 1180 1200	1180	1190	1200
reecaga	ATGTGGAA	AAGTTATGG	GGAAAAGGAJ	TAAAATGGTTG	TCAACCCAATCTTTCACGCAAGCTGGCAGAAGGTTATGGGGAAAAGGATAAAATGGTTGATGGTGAGCAAGTAATCACTAAAAATGACATTATT	AGTAATCACT	FAAAATGAC?	TTATT
1230 \AACAAA) 1 3 1 1 1	1240 AGTATCTGC	1250 ATTGATAAA	1210 1220 1230 1240 1250 1260 1270 1270 1290 1300 1300 1300 1210 1290 1300 1300 1200 1300 1300 1300	1270 GCCATTTCCAA	1280 ATATCTAAA	1290 FTGTCAACTC	1300 AGTAA

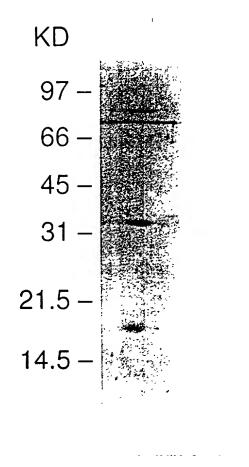
1310 1320 AAAAAAAAAAAAAACTCGAG FIG. 2B

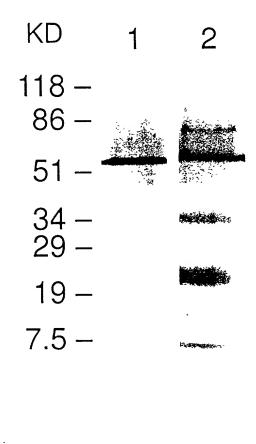




F16. 3A

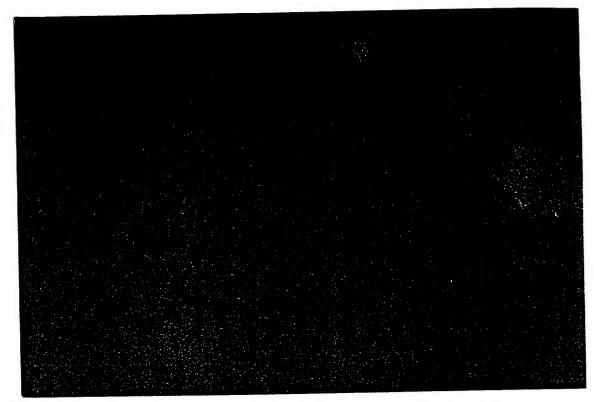
F16 3B



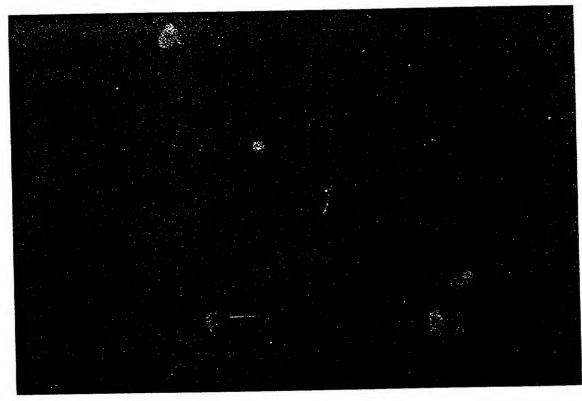


F16. 4A

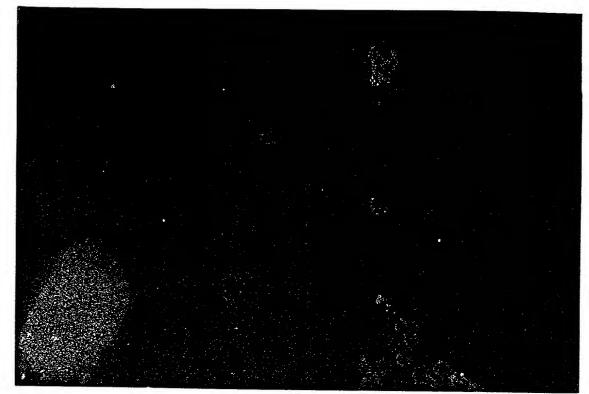
F16, 4B



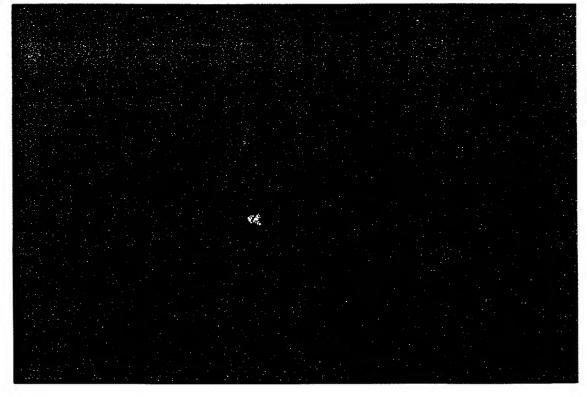
F16. 5A



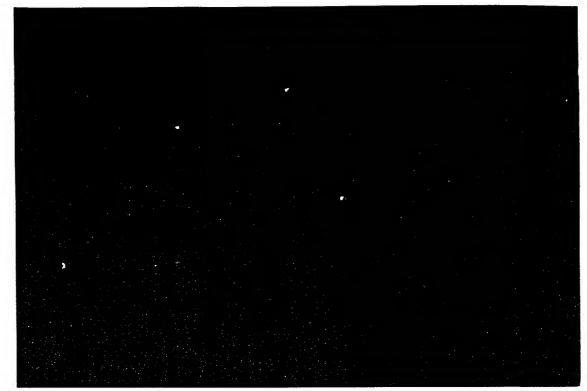
F16. 5E



F16 5C



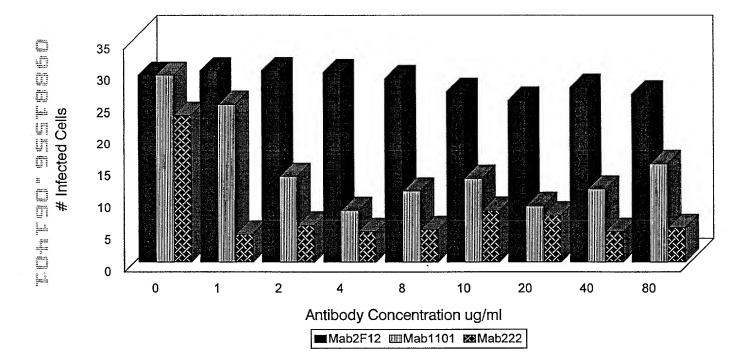
#16 5D



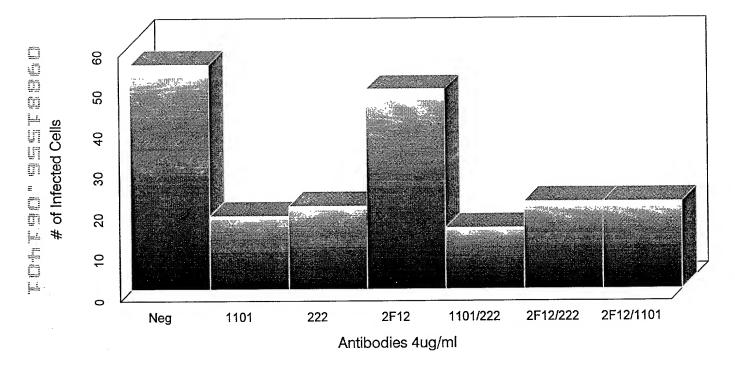
F16 5E



F16 5F



F16.6



F16. 7